? b 155,50,357
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$0.33 0.095 DialUnits File1
$0.33 Estimated cost File1
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$0.36 Estimated cost this search
$0.36 Estimated total session cost 0.095 DialUnits

SYSTEM:OS - DIALOG OneSearch
File 155:MEDLINE(R) 1966-2003/Mar W1
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File 50:CAB Abstracts 1972-2003/Jan
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*File 50: Truncating CC codes is recommended for full retrieval.
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File 357:Derwent Biotech Res. _1982-2003/Mar W2
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Set Items Description
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? s autonomous and parvo?
12082 AUTONOMOUS
12032 PARVO?
S1 255 AUTONOMOUS AND PARVO?
? s terminus or termini or telomer? or end or ends
47649 TERMINUS
11637 TERMINI
12021 TELOMER?
326243 END
33960 ENDS
S2 412462 TERMINUS OR TERMINI OR TELOMER? OR END OR ENDS
? s s1 and s2
255 S1
412462 S2
S3 56 S1 AND S2
? rd
...examined 50 records (50)
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S4 47 RD (unique items)
? t s4/7/1 3 10 11 14-18 20 26 37 42 45 46
4/7/1 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.
14021231 22302490 PMID: 12413415
Autonomous parvovirus vectors.
Maxwell Ian H; Terrell Kristina L; Maxwell Francoise; et al
Department of Dermatology and University of Colorado Cancer Center, University of Colorado Health Sciences Center, 4200 East Ninth Avenue, Denver, CO 80262, USA. ian.maxwell@uchsc.edu
Methods (San Diego, Calif.) (United States) Oct 2002, 28 (2) p168-81 , ISSN 1046-2023 Journal Code: 9426302
Contract/Grant No.: AI42766; AI; NIAID; AR48388; AR; NIAMS; +
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: In Process
Parvoviruses are small, icosahedral viruses (approximately 25 nm) containing a single-strand DNA genome (approximately 5 kb) with hairpin termini. Autonomous parvoviruses (APVs) are found in many species; they do not require a helper virus for replication but they do require proliferating cells (S-phase functions) and, in some cases, tissue-specific factors. APVs can protect animals from spontaneous or experimental tumors, leading to consideration of these viruses, and vectors derived from them, as anticancer agents. Vector development has focused on three rodent APVs that can infect human cells, namely, LuIII, MVM, and H1. LuIII-based vectors with complete replacement of the viral coding sequences can direct transient or persistent expression of transgenes in cell culture. MVM-based and H1-based vectors with substitution of transgenes for the viral capsid sequences retain viral nonstructural (NS) coding sequences and express the NS1 protein. The latter serves to amplify the vector genome in target cells, potentially contributing to antitumor activity. APV vectors have packaging capacity for foreign DNA of approximately 4.8 kb, a limit that probably cannot be exceeded by more than a few percent. LuIII vectors can be pseudotyped with capsid proteins from related APVs, a promising strategy for controlling tissue tropism and circumventing immune responses to repeated administration. Initial success has been achieved in targeting such a pseudotyped vector by genetic modification of the capsid. Subject to advances in production and purification methods, APV vectors have potential as gene transfer agents for experimental and therapeutic use, particularly for cancer therapy. Copyright 2002 Elsevier Science (USA)
Record Date Created: 20021104

4/7/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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10378075 99355161 PMID: 10428207
cis requirements for the efficient production of recombinant DNA vectors based on autonomous parvoviruses.
Kestler J; Neeb B; Struyf S; Van Damme J; Cotmore S F; D'Abramo A; Tattersall P; Rommelaere J; Dinsart C; Cornelis J J
Applied Tumor Virology Abt. F0100 and INSERM U375 Deutsches Krebsforschungszentrum, Heidelberg, Germany.

Human gene therapy (UNITED STATES) Jul 1 1999, 10 (10) p1619-32, ISSN 1043-0342 Journal Code: 9008950
Contract/Grant No.: CA29303; CA; NCI
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

The replication of viral genomes and the production of recombinant viral vectors from infectious molecular clones of parvoviruses MVMp and H1 were greatly improved by the introduction of a consensus NS-1 nick site at the junction between the left-hand viral terminus and the plasmid DNA. Progressive deletions of up to 1600 bp in the region encoding the structural genes as well as insertions of foreign DNA in replacement of those sequences did not appreciably affect the replication ability of the recombinant H1 virus genomes. In contrast, the incorporation of these genomes into recombinant particles appeared to depend on in cis-provided structural gene sequences. Indeed, the production of H1 viral vectors by cotransfection of recombinant clones and helper plasmids providing the structural proteins (VPs) in trans, drastically decreased when more than 800 bp was removed from the VP transcription unit. Furthermore, titers of viral vectors, in which most of the VP-coding region was replaced by an equivalent-length sequence consisting of reporter cDNA and stuffer DNA, were reduced more than 50 times in comparison with recombinant vectors in which stuffer DNA was not substituted for the residual VP sequence. In addition, viral vector production was restricted by the overall size of the genome, with a mere 6% increase in DNA length leading to an approximately 10 times lower encapsidation yield. Under conditions fulfilling the above-mentioned requirements for efficient packaging, titers of virus vectors from improved recombinant molecular DNA clones amounted to 5 x 10(7) infectious units per milliliter of crude extract. These titers should allow the assessment of the therapeutic effect of recombinant parvoviruses expressing small transgenes in laboratory animals.

Record Date Created: 19990922

4/7/10 (Item 10 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09588055 98007643 PMID: 9349487

The minute virus of mice (MVM) nonstructural protein NS1 induces nicking of MVM DNA at a unique site of the right-end telomere in both hairpin and duplex conformations in vitro.

Willwand K; Baldauf A Q; Deleu L; Mumtsidu E; Costello E; Beard P; Rommelaere J

Deutsches Krebsforschungszentrum, Department of Applied Tumor Virology, and Formation INSERM U375, Heidelberg, Germany. k.willwand@dkfz-heidelberg.de

Journal of general virology (ENGLAND) Oct 1997, 78 (Pt 10) p2647-55, ISSN 0022-1317 Journal Code: 0077340
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

The right-end telomere of replicative form (RF) DNA of the autonomous parvovirus minute virus of mice (MVM) consists of a sequence that is self-complementary except for a three nucleotide loop around the axis of symmetry and an interior bulge of three unpaired nucleotides on one strand (designated the right-end 'bubble'). This right-end inverted repeat can exist in the form of a folded-back strand (hairpin conformation) or in an extended form, base-paired to a copy strand (duplex conformation). We recently reported that the right-end telomere is processed in an A9 cell extract supplemented with the MVM nonstructural protein NS1. This processing is shown here to result from the NS1-dependent nicking of the complementary strand at a unique position 21 nt inboard of the folded-back genomic 5' end. DNA species terminating in duplex or hairpin configurations, or in a mutated structure that has lost the right-end bulge, are all cleaved in the presence of NS1, indicating that features distinguishing these structures are not prerequisites for nicking under the in vitro conditions tested. Cleavage of the hairpin structure is followed by strand-displacement synthesis, generating the right-end duplex conformation, while processing of the duplex structure leads to the release of free right-end telomeres. In the majority of molecules, displacement synthesis at the right terminus stops a few nucleotides before reaching the end of the template strand, possibly due to NS1 which is covalently bound to this end. A fraction of the right-end duplex product undergoes melting and re-folding into hairpin structures (formation of a 'rabbit-ear' structure).

Record Date Created: 19971117

4/7/11 (Item 11 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09268918 97151079 PMID: 8995615

Specific initiation of replication at the right-end telomere of the closed species of minute virus of mice replicative-form DNA.

Baldauf A Q; Willwand K; Mumtsidu E; Nuesch J P; Rommelaere J

Department of Applied Tumor Virology, Deutches Krebsforschungszentrum, Heidelberg, Germany.

Journal of virology (UNITED STATES) Feb 1997, 71 (2) p971-80, ISSN 0022-538X Journal Code: 0113724
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

We have developed an in vitro system that supports the replication of

natural DNA templates of the autonomous parvovirus minute virus of mice (MVM). MVM virion DNA, a single-stranded molecule bracketed by short, terminal, self-complementary sequences, is converted into double-stranded replicative-form (RF) DNA when incubated in mouse A9 fibroblast extract. The 3' end of the newly synthesized complementary strand is ligated to the right-end hairpin of the virion strand, resulting in the formation of a covalently closed RF (cRF) molecule as the major conversion product. cRF DNA is not further replicated in A9 cell extract alone. On addition of purified MVM nonstructural protein NS1 expressed from recombinant baculoviruses or vaccinia viruses, cRF DNA is processed into a right-end (5' end of the virion strand) extended form (5'eRF). This is indicative of NS1-dependent nicking of the right-end hairpin at a distinct position, followed by unfolding of the hairpin and copying of the terminal sequence. In contrast, no resolution of the left-end hairpin can be detected in the presence of NS1. In the course of the right-end nicking reaction, NS1 gets covalently attached to the right-end telomere of the DNA product, as shown by immunoprecipitation with NS1-specific antibodies. The 5'eRF product is the target for additional rounds of NS1-induced nicking and displacement synthesis at the right end, arguing against the requirement of the hairpin structure for recognition of the DNA substrate by NS1. Further processing of the 5'eRF template in vitro leads to the formation of dimeric RF (dRF) DNA in a left-to-left-end configuration, presumably as a result of copying of the whole molecule by displacement synthesis initiated at the right-end telomere. Formation of dRF DNA is highly stimulated by NS1. The experimental results presented in this report support various assumptions of current models of parvovirus DNA replication and provide new insights into the replication functions of the NS1 protein.

Record Date Created: 19970218

4/7/14 (Item 14 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07865779 94002366 PMID: 8399491

Recombinant LuIII autonomous parvovirus as a transient transducing vector for human cells.

Maxwell I H; Maxwell F; Rhode S L; Corsini J; Carlson J O
University of Colorado Cancer Center, Denver 80262.

Human gene therapy (UNITED STATES) Aug 1993, 4 (4) p441-50, ISSN 1043-0342 Journal Code: 9008950
Contract/Grant No.: CA50285; CA; NCI
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

Recombinants based on the genome of the autonomous parvovirus, LuIII, were constructed by replacing the viral coding sequences in an infectious clone (pGLu883) by a luciferase or beta-galactosidase reporter, which was linked to the viral P4 promoter. In cells cotransfected with either of these constructs, together with a plasmid supplying LuIII nonstructural and capsid proteins, excision and replication of the recombinant genome occurred. Transducing virions accumulated in the culture medium of the cotransfected cells, as assayed by reporter activity in recipient cells exposed to this medium. Transducing activity could be neutralized by antiserum to LuIII. Production of replicative form DNA and transducing virions were observed following cotransfection of HeLa, 293, or NB324K cells, in increasing order of efficiency. When homology existed between the recombinant genome and sequences flanking the viral genes in the helper construct, concomitant production of replication-competent, cytopathic virus was sometimes observed. This could be minimized by removal of the left end homology from the helper; by this means, preparations of luciferase transducing virus were obtained free from replication-competent virus. With such preparations, we observed luciferase expression (declining after 3 days) for up to 7 days in recipient HeLa cells. Hybridization of the recombinant viral DNA with strand-specific luciferase probes indicated packaging of both strands (as reported for LuIII), but with a several-fold excess of the (-) strand. We suggest that transducing-autonomous parvoviruses will be useful in gene transfer applications, possibly including gene therapy when only transient expression is desired.

Record Date Created: 19931123

4/7/15 (Item 15 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06892959 91202123 PMID: 2016597

Construction and nucleotide sequence analysis of an infectious DNA clone of the autonomous parvovirus, mink enteritis virus.

Kariatsumari T; Horiuchi M; Hama E; Yaguchi K; Ishigurio N; Goto H; Shinagawa M
Department of Veterinary Public Health, Faculty of Veterinary Medicine, Obihiro University of Agriculture and Veterinary Medicine, Hokkaido, Japan.

Journal of general virology (ENGLAND) Apr 1991, 72 (Pt 4) p867-75, ISSN 0022-1317 Journal Code: 0077340
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed

We have cloned the replicative form (RF-) DNA of mink enteritis virus (MEV), constructed an infectious recombinant plasmid containing MEV DNA and determined the nucleotide sequence of the cloned MEV DNA. RF-DNAs were detected and infectious virus was generated when the recombinant plasmid containing the entire MEV genome was introduced into feline kidney cell cultures. The MEV genome was 5094 nucleotides (nt) in length; the 3' end of the virion strand contained a 205 nt palindromic sequence and the 5' end a 62 nt palindromic sequence that could assume Y- and U-shaped

configurations, respectively. The 5' end of the virion strand had a direct repeat of 61 nt at the carboxyl terminus of the capsid protein gene. The organization of the MEV genome is similar to those of canine parvovirus (CPV) and feline panleukopenia virus (FPLV); there are two large open reading frames (ORFs), one in the 3' half and the other in the 5' half of the genome, with coding capacities of 668 and 722 amino acid residues, respectively. Both are in the same reading frame and no significant ORFs are apparent in the virion strand (negative-sense strand). Possible functional promoter motifs are located at map unit (m.u.) 4.5 and m.u. 40, and a possible functional poly(A) signal is located at m.u. 96. The nucleotide and amino acid sequence homology with CPV and FPLV is greater than 98%, consistent with the hypothesis that MEV and CPV are host-range variants of FPLV.
Record Date Created: 19910523

4/7/16 (Item 16 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06701124 91012793 PMID: 2145445
Interaction of virally coded protein and a cell cycle-regulated cellular protein with the bovine parvovirus left terminus ori.
Metcalf J B; Bates R C; Lederman M
Biology Department, Virginia Polytechnic Institute and State University, Blacksburg 24061-0406.
Journal of virology (UNITED STATES) Nov 1990, 64 (11) p5485-90, ISSN 0022-538X Journal Code: 0113724
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Replication of parvoviruses requires cis signals located in terminal palindromes that function as origins of replication in conjunction with trans-acting viral and cellular proteins. A gel retardation assay was used to identify proteins in crude nuclear extracts of bovine parvovirus (BPV)-infected bovine fetal lung cells that interact with the hairpinned left end (3' OH terminus of the viral minus strand in the flop conformation) of BPV. Three specific DNA-protein complexes formed. One complex was shown to involve a BPV structural protein(s) by inhibiting its formation when antiserum specific for these BPV proteins was used. By specific competition with serum containing antibodies against the BPV nonstructural proteins, a second complex was shown to involve a BPV nonstructural protein. A third complex contained protein of cellular origin and was also formed with extracts of uninfected bovine fetal lung cells. DNA competition assays suggest that the viral proteins do not bind to the right hairpin, which differs in sequence and secondary structure from the left terminus, or to a BPV terminus that lacks the first 52 nucleotides, preventing formation of the stem of the hairpin. The cellular protein is regulated in a cell cycle-dependent fashion, with its binding activity increased in uninfected, actively dividing cells compared with contact-inhibited cells. Since autonomous parvovirus replication requires an S-phase factor for progeny formation, the terminal binding protein demonstrated here is a candidate for this factor.
Record Date Created: 19901115

4/7/17 (Item 17 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06620247 90320152 PMID: 2371779
Construction of an infectious genomic clone of porcine parvovirus: effect of the 5'-end on DNA replication.
Casal J I; Diaz-Aroca E; Ranz A I; Manclus J J
Inmunologia y Genetica Aplicada, S.A. (Ingenasa), Madrid, Spain.
Virology (UNITED STATES) Aug 1990, 177 (2) p764-7, ISSN 0042-6822 Journal Code: 0110674
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
The linear single-stranded DNA genome of the porcine parvovirus, an autonomous parvovirus, was cloned in duplex form into the bacterial plasmid pUC18 using a simple and reliable method. These clones were stable during propagation in Escherichia coli JM109. The recombinant clones of porcine parvovirus were infectious when transfected into monolayers of swine testes cells as identified by the development of cytopathic effect, indirect immunofluorescence with specific antiserum, and hemagglutination assays. DNA isolated from progeny virus arising from transfected infectious clones was found to be indistinguishable from wild-type DNA by restriction enzyme analysis. Defective genomes could also be detected in the progeny DNA even though the infection was initiated with homogeneous, cloned DNA. The presence of the turn of the 5'-end loop seems to be necessary to get stable infectious clones.
Record Date Created: 19900821

4/7/18 (Item 18 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06373299 90066086 PMID: 2586345
Characterization of replicative form DNA of the autonomous parvovirus mink enteritis virus.
Shinagawa M; Nomura Y; Kariatumari T; Ishiguro N; Horiuchi M; Goto H
Department of Veterinary Public Health, School of Veterinary Medicine, Obihiro University of Agriculture.
Microbiology and immunology (JAPAN) 1989, 33 (9) p721-32, ISSN 0385-5600 Journal Code: 7703966

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Characterization of replicative form (RF) DNA of mink enteritis virus (MEV) was carried out. Most of the RF DNA were bound to terminal protein but some were free from the protein. The protein-free RF DNA increased about 7 times from 30 to 50 hr post-infection, while the DNA with protein increased less. The molecules of the replicative intermediate which were partially single-stranded DNA and bound to terminal protein were present. Two terminal conformations, "extended" and "turnaround," were observed in both ends of both terminal protein-bound and protein-free RF DNA. The 5' end labeling revealed that 5' ends of protein-free RF DNA were not blocked to phosphorylation by an amino acid or an oligopeptide which attaches to 5' ends of proteolytically deproteinized RF DNA. Restriction analysis of incomplete RF DNA which was partially double-stranded DNA showed that extended conformation was dominant in such incomplete RF molecules.
Record Date Created: 19891227

4/7/20 (Item 20 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06294452 89382767 PMID: 2528644
Both excision and replication of cloned autonomous parvovirus DNA require the NS1 (rep) protein.
Rhode S L
Eppley Institute, University of Nebraska Medical Center, Omaha 68105-1065.
Journal of virology (UNITED STATES) Oct 1989, 63 (10) p4249-56, ISSN 0022-538X Journal Code: 0113724
Contract/Grant No.: CA36727; CA; NCI
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
When a bacterial plasmid containing the entire genome of LuIII virus except for the terminal 18 nucleotides from the right end is transfected into HeLa cells, the viral DNA is rescued and replicated, with production of infectious virus. This experimental system was used to examine the viral proteins and cis elements required for the excision and replication of viral DNA. The deletion of the entire NS1 gene provided a viral genome that was excised from the plasmid and replicated only when an NS1 gene was provided in trans. A frameshift mutation in the NS2 intron that truncates NS1 prevented excision and replication. Deletion of the left-end terminal inverted repeat or the right-end inverted repeat prevented excision of viral DNA from that end but not from the wild-type terminus. The viral terminus excised from the plasmid was protected from a processive degradation process, which began on the vector portion of the plasmid. The inhibitor of DNA polymerases alpha and delta, aphidicolin, blocked the excision reaction.
Record Date Created: 19891017

4/7/26 (Item 26 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05670611 88091050 PMID: 3275788
Genomic clones of bovine parvovirus: construction and effect of deletions and terminal sequence inversions on infectivity.
Shull B C; Chen K C; Lederman M; Stout E R; Bates R C
Department of Biology, Virginia Polytechnic Institute and State University, Blacksburg 24061-0794.
Journal of virology (UNITED STATES) Feb 1988, 62 (2) p417-26, ISSN 0022-538X Journal Code: 0113724
Contract/Grant No.: RRO-7095; RR; NCRR
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Genomic clones of the autonomous parvovirus bovine parvovirus (BPV) were constructed by blunt-end ligation of reannealed virion plus and minus DNA strands into the plasmid pUC8. These clones were stable during propagation in Escherichia coli JM107. All clones tested were found to be infectious by the criteria of plaque titer and progressive cytopathic effect after transfection into bovine fetal lung cells. Sequencing of the recombinant plasmids demonstrated that all of the BPV inserts had left-end (3')-terminal deletions of up to 34 bases. DNA isolated from progeny virions arising from transfected infectious clones was found to be indistinguishable from wild-type DNA by restriction enzyme analysis. Defective genomes could also be detected in the progeny DNA even though the infection was initiated with homogenous, cloned DNA. Full-length genomic clones with 3' flip and 3' flop conformations were constructed and were found to have equal infectivity. Analysis of low-molecular-weight DNA isolated from lysates of cells transfected with these clones demonstrated that rescue and replication of BPV DNA could be detected 3 to 8 days after transfection. Expression of capsid proteins from transfected genomes was demonstrated by hemagglutination, indirect immunofluorescence, and immunoprecipitation of [35S]methionine-labeled cell lysates. Use of appropriate antiserum for immunoprecipitation showed the synthesis of BPV capsid and noncapsid proteins after transfection. Independently, a series of genomic clones with increasingly larger 3'-terminal deletions was prepared from separately subcloned 3'-terminal fragments. Transfection of these clones into bovine fetal lung cells revealed that deletions of up to 34 bases at the 3' end lowered but did not abolish infectivity, while deletions of greater than 52 bases were lethal. End-label analysis showed

that the 34-base deletion was repaired to wild-type length in the progeny virus.
Record Date Created: 19880220

4/7/37 (Item 37 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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04246254 83241927 PMID: 6345805
Construction of an infectious molecular clone of the autonomous parvovirus minute virus of mice.
Merchlinsky M J; Tattersall P J; Leary J J; Cotmore S F; Gardiner E M; Ward D C
Journal of virology (UNITED STATES) Jul 1983, 47 (1) p227-32, ISSN 0022-538X Journal Code: 0113724
Contract/Grant No.: CA-16038; CA; NCI; CA-29303; CA; NCI; GM-20124; GM; NIGMS
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
The linear single-stranded DNA genome of minute virus of mice, an autonomous parvovirus, was cloned in duplex form into the bacterial plasmid pBR322. The recombinant clones of minute virus of mice were infectious when transfected into monolayers of human 324K cells and produced virus plaques with an efficiency of about 6% that obtained with duplex replicative-form DNA purified from cells infected with minute virus of mice. Southern blot analysis of transfected cells indicated that the cloned minute virus of mice genome requires both termini to be intact for excision and replication as a linear duplex molecule.
Record Date Created: 19830811

4/7/42 (Item 42 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.
03186483 80001961 PMID: 225040
Structure of the 3' hairpin termini of four rodent parvovirus genomes: nucleotide sequence homology at origins of DNA replication.
Astell C R; Smith M; Chow M B; Ward D C
Cell (UNITED STATES) Jul 1979, 17 (3) p691-703, ISSN 0092-8674 Journal Code: 0413066
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
The nucleotide sequences of the 3' termini of the DNA from four autonomous rodent parvoviruses have been determined. The terminus of each genome exists as a Y-shaped hairpin structure involving 115 or 116 nucleotides. The sequence of this region of DNA is highly conserved and shows no evidence of internal sequence heterogeneity, a characteristic which is observed in the terminal nucleotide sequence of the helper-dependent, adeno-associated viruses (Berns et al., 1978a). The implications of these results with respect to the models of parvovirus DNA replication are discussed.
Record Date Created: 19791129

4/7/45 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.
(c) 2003 Thomson Derwent & ISI. All rts. reserv.
0209359 DBR Accession No.: 97-04480 PATENT
Recombinant vectors based on parvo virus nucleic acids - parvo virus vector for use in cancer gene therapy
AUTHOR: Rhode S L; Maxwell F
CORPORATE SOURCE: USA.
PATENT ASSIGNEE: Univ.Colorado-Found. 1996
PATENT NUMBER: US 5585254 PATENT DATE: 961217 WPI ACCESSION NO.: 97-064348 (9706)
PRIORITY APPLIC. NO.: US 685628 APPLIC. DATE: 910415
NATIONAL APPLIC. NO.: US 685628 APPLIC. DATE: 910415
LANGUAGE: English
ABSTRACT: A recombinant vector contains nucleic acid sequences of an autonomous parvo virus (AP) joined to at least 1 foreign nucleic acid sequence. The AP sequences comprise functional left and right end inverted terminal repeats enclosing the foreign sequence, which is located between them. Also claimed are: a recombinant virus particle comprising a vector packaged in an autonomous parvo virus capsid; a helper construct plasmid pSVLu; and a method for producing a recombinant virus particle for delivery of a gene to a targeted cell, which involves cotransfecting a host cell with a vector and a helper construct that effects amplification of the vector and/or packaging of the vector in a parvo virus capsid and culturing the transfected host cell. The vector is used as a delivery vehicle for gene therapy, especially for restoring the function of a defective gene or for expressing a cytotoxic agent to destroy cancer cells or pathogen-infected cells and for production of the RNA or protein encoded by the heterologous nucleic acid sequence (all claimed). (26pp)

4/7/46 (Item 2 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.
(c) 2003 Thomson Derwent & ISI. All rts. reserv.
0062436 DBR Accession No.: 87-06784
Complete nucleotide sequence and genome organization of bovine parvo virus - cattle virus DNA sequence, application to vaccine development
AUTHOR: Chen K C; Shull B C; Moses E A; Lederman M; Stout E R; Bates R C

CORPORATE SOURCE: Department of Biology, Virginia Polytechnic Institute and State University, Blacksburg, Virginia 24061, U.S.A.
JOURNAL: J.Virol. (60, 3, 1085-97) (196
CODEN: JOVIAM
LANGUAGE: English
ABSTRACT: The complete nucleotide sequence of bovine parvo virus (BPV), and autonomous parvo virus, has been determined. BPV was propagated in cattle fetal lung cells and single-stranded DNA was purified from the cells by centrifugation of disrupted cells on a CsCl gradient, followed by serine protease (EC-3.4.21.14) digestion, phenol-chloroform extraction and ethanol precipitation. The purified DNA was replicated to a double-stranded form and cloned in pUC plasmids and M13 phages in Escherichia coli JM107 and in pAT153 plasmids in E. coli HB101. DNA from these sources was sequenced by the chain termination method. The sequence consisted of 5,491 nucleotides with nonidentical imperfect palindromic sequences at the termini. In the plus strand, there were 3 large open reading frames encoding 729, 255, and 685 amino acids respectively. The sequence was further characterized. The highly conserved amino acid sequences of the parvo viruses may be useful for vaccine design. (55 ref)
? s mvm or h1 or luiii or lu111
357 MVM
21351 H1
42 LUIII
0 LU111
S5 21735 MVM OR H1 OR LUIII OR LU111
? s left or right
274608 LEFT
207529 RIGHT
S6 394366 LEFT OR RIGHT
? s s5 and s6 not s3
21735 S5
394366 S6
56 S3
S7 528 S5 AND S6 NOT S3
? s vector? and s7
214759 VECTOR?
528 S7
S8 16 VECTOR? AND S7
? rd
...completed examining records
S9 16 RD (unique items)
? t s9/7/3
9/7/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2003 The Dialog Corp. All rts. reserv.
09188938 97083335 PMID: 8929909

Autonomous parvovirus transduction of a gene under control of tissue-specific or inducible promoters.
Maxwell I H; Spitzer A L; Long C J; Maxwell F
University of Colorado Cancer Center and Health Sciences Center, Denver 80262, USA.
Gene therapy (ENGLAND) Jan 1996, 3 (1) p28-36, ISSN 0969-7128
Journal Code: 9421525
Contract/Grant No.: CA-50285; CA; NCI
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Several classes of viruses are in use, or are being developed, as gene therapy vectors. Viruses with small genomes containing few essential genes have the advantage of requiring only simple complementation systems to allow packaging of foreign DNA, substituted for the entire viral coding sequences. Retroviruses and the dependent parvovirus AAV (adeno-associated virus) have been used in this way, and both possess an efficient integration mechanism which should allow long-term expression of transduced genes. In some situations, however, long-term persistence may be undesirable and there is a need for small, non-integrating viral vectors. Autonomous parvoviruses, such as LuIII, have potential as such vectors for short-term expression of therapeutic genes. We previously described recombinants of LuIII that transduced reporter genes, expressed using the viral constitutive promoter, P4. We have now generated several recombinants containing regulated promoters. A virus including a liver-specific enhancer directed 10- to 20-fold preferential expression of the luciferase reporter in transduced human hepatoma (HepG2) versus HeLa cells. In additional LuIII recombinants, the luciferase reporter was linked with chimeric promoters containing binding sequences for either the yeast GAL4 protein or the bacterial tetracycline repressor. Luciferase expression was strongly activated when these viruses were used to infect cells containing a cognate trans-activator (GAL4 or tTA, a tetracycline repressor fusion with VP16 of herpes simplex), introduced by transfection. The response to tTA could be abolished, or reduced in a graded manner, by exposure of the infected cells to tetracycline. Further results suggested that an increase in basal expression, apparently mediated by the viral left terminal inverted repeat, could be minimized by interposing polyadenylation signals between this sequence and the promoter. These results confirm that appropriate transcriptional regulation can be achieved for genes transduced by an autonomous parvovirus vector. Such vectors therefore show promise for the delivery of therapeutic genes in situations requiring cell-specific, short-term expression, eg in targeting suicide genes for ablation of cancer cells.
Record Date Created: 19970328
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